

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2002, 16:48:39 ; Search time 4873.04 Seconds  
(without alignments)  
1604.679 Million cell updates/sec

Title: us-09-236-995d-3  
Perfect score: 474  
Sequence: 1 acaagatgtattatggca.....gtttccatcacaaagaggtag 474

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: gb.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.om.\*

20: em.or.\*

21: em.ov.\*

22: em.pat.\*

23: em.ph.\*

24: em.pl.\*

25: em.ro.\*

26: em.sts.\*

27: em.sy.\*

28: em.un.\*

29: em.vi.\*

30: em.htgo\_hum.\*

31: em.htgo\_inv.\*

32: em.htgo\_rod.\*

33: em.htg\_hum.\*

34: em.htg\_inv.\*

35: em.htg\_rod.\*

36: em.htg\_other.\*

Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di

#### SUMMARIES

Result No. Score Match Length DB ID Description

|    |       |       |        |    |            |                     |
|----|-------|-------|--------|----|------------|---------------------|
| 1  | 474   | 100.0 | 3211   | 8  | ZMPARP2    | AJ222589 Zea mays   |
| 2  | 474   | 100.0 | 3285   | 8  | AF093627   | AF093627 Zea mays   |
| 3  | 280   | 59.1  | 3187   | 8  | AFH131705  | AFH131705 Arabidops |
| 4  | 158.6 | 33.5  | 1939   | 10 | RNPARP2    | X65457 R.norvegicu  |
| 5  | 157.6 | 33.2  | 3718   | 5  | XELPADPRP  | D14667 Frog mrna f  |
| 6  | 157   | 33.1  | 3128   | 10 | RNU94340   | U94340 Rattus norv  |
| 7  | 155   | 32.7  | 3617   | 5  | XLPA3PG    | Z12139 X.laavis PA  |
| 8  | 154.4 | 32.6  | 2147   | 8  | ATPARP     | Z48243 A.thaliana   |
| 9  | 153.8 | 32.4  | 3036   | 5  | GGPADPRP   | X52690 Chicken mRN  |
| 10 | 152.2 | 32.1  | 3845   | 10 | GC012041   | GC012041 Mus muscu  |
| 11 | 151.4 | 31.9  | 2295   | 8  | ZMPARP1    | AJ222588 Zea mays   |
| 12 | 150.6 | 31.8  | 3172   | 10 | MMADPRP    | X14206 Mouse mrna   |
| 13 | 150.6 | 31.8  | 3589   | 4  | BOVPAS     | D90073 Bovine poly  |
| 14 | 149   | 31.4  | 1732   | 10 | AF126717   | AF126717 Mus muscu  |
| 15 | 147.4 | 31.1  | 3047   | 10 | AF168781   | AF168781 Crictetulu |
| 16 | 142.6 | 30.1  | 1771   | 9  | HUMADPRP   | M17081 Human place  |
| 17 | 142.6 | 30.1  | 3640   | 9  | HUMPOLP    | M18112 Human poly(  |
| 18 | 142.6 | 30.1  | 3792   | 6  | A52134     | A52134 Sequence 1   |
| 19 | 142.6 | 30.1  | 3795   | 9  | HUMRISDAD  | J03473 Human poly(  |
| 20 | 142.6 | 30.1  | 5787   | 9  | GORADPRB   | L24094 Gorilla gor  |
| 21 | 139.4 | 29.4  | 3045   | 6  | AX058340   | AX058340 Sequence   |
| 22 | 139.4 | 29.4  | 3660   | 9  | HUMPPOL    | AX062277 Sequence   |
| 23 | 139.4 | 29.4  | 3747   | 6  | I14359     | M32721 Human poly(  |
| 24 | 139.4 | 29.4  | 1822   | 3  | DMPARP5    | I14359 Sequence 5   |
| 25 | 137.8 | 29.1  | 2682   | 9  | S54638     | AF051548 drosophill |
| 26 | 137.8 | 29.1  | 3080   | 3  | DROADPRPA  | S54638 (pseudogene  |
| 27 | 137.8 | 29.1  | 5345   | 6  | I14360     | D13806 Fruit fly m  |
| 28 | 137.8 | 29.1  | 9254   | 9  | HUMPADPRP2 | I14360 Sequence 7   |
| 29 | 137.8 | 29.1  | 10988  | 2  | AE014613   | L14752 Homo sapien  |
| 30 | 137.8 | 29.1  | 16864  | 3  | AE002892   | AC014613 Drosophill |
| 31 | 137.8 | 29.1  | 155026 | 9  | AL442128   | AE002892 Drosophill |
| 32 | 137.8 | 29.0  | 3463   | 3  | SPEPADPRP  | AL442128 Human DNA  |
| 33 | 137.4 | 28.7  | 2682   | 6  | I14357     | D16482 Sarcophaga   |
| 34 | 136.2 | 25.9  | 687    | 6  | AX058382   | I14357 Sequence 3   |
| 35 | 122.6 | 25.9  | 738    | 6  | AX058380   | AX058382 Sequence   |
| 36 | 122.6 | 25.9  | 864    | 6  | AX058336   | AX058380 Sequence   |
| 37 | 122.6 | 25.9  | 1754   | 9  | HS236912   | AX058336 Sequence   |
| 38 | 122.6 | 25.9  | 1797   | 9  | HS236876   | AJ236912 Homo sapi  |
| 39 | 122.6 | 25.9  | 1814   | 6  | AX058317   | AJ236876 Homo sapi  |
| 40 | 122.6 | 25.9  | 1843   | 6  | AX008892   | AX058317 Sequence   |
| 41 | 122.6 | 25.9  | 1874   | 6  | AX058374   | AX008892 Sequence   |
| 42 | 122.6 | 25.9  | 3200   | 6  | AX058362   | AX058374 Sequence   |
| 43 | 122.6 | 25.5  | 1910   | 9  | AF085734   | AX058362 Sequence   |
| 44 | 121   | 25.5  | 1707   | 6  | AX058338   | AF085734 Homo sapi  |
| 45 | 120.2 | 25.4  |        |    |            | AX058338 Sequence   |

#### ALIGNMENTS

#### RESULT 1

ZMPARP2 ZMPARP2 3211 bp mrna PLN 19-NOV-1997  
LOCUS Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp).  
DEFINITION  
ACCESSION AJ222589  
VERSION AJ222589.1 GI:2632128  
KEYWORDS PARP gene; poly(ADP-ribose) polymerase;  
SOURCE Zea mays.  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 3211)  
Babychuk,E., Cottrell,P., Storozhenko,S., Fuangthong,M.,  
O'Farrell,M., Van Montagu,M., Inze,D. and Kushnir,S.

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### REFERENCE

#### AUTHORS

#### TITLE

#### Direct Submission

JOURNAL Submitted (14-NOV-1997) Kushnir S., VIB, Dep. Genetics, Ledegancstraet 35, Gent, B9000, Belgium

FEATURES

source Location/Qualifiers

1. .3211 /organism="Zea mays" /db\_xref="taxon:4577" 113. .3022 /gene="PARP" 113. .3022 /gene="PARP" /function="secondary protein modification" /codon\_start=1 /product="poly(ADP-ribose) polymerase" /protein\_id="CAA10889.1" /db\_xref="GI:2632129" /db\_xref="SPREMBL:024570" /translation="MAAPRAKAWAEYAKSGRACKSCRSPIAKDQLRLGKMWQASQFD GFPMNHNHSDVDDGIDALRWDDQEKIRNYVGSASAGTSTAAPPEKCTIETAPAR TSCRCSEKTKGSRVLSAKLESSEKPGKIPWYHANCFFEVSPSATVEKSGWGLTDE DRKRLDGLKDVGNFONKSGRKKSENDIDSVKARLDESTSEGVNKGGLVDPDR GSNTSSADIDQLKKEQSDTLKLDGLKTHVSAELRDLMEANGQDTSGERHLLDRC ADGHIFGALGPCVPCANGMYIYNGYOCSGNVSEWSEKCTISATEPVRVKKWQIPGRT KNDYLMKWFQSKRPKPEVLPMPSPKSGSKATQRTSLSSKGLDKLRVSVVQSKKE AANFMIEKLIAGLAFYARVVKDIDCLACGELDNENAEYRKARLKIPIVREGYIGE CVKKNKMLPFDLYKLENALSSKSTVTYVVKGRSAVHESGSLQDTAHILEDKSIYN ATLNMSDLALGVNSYYVLIQIEQDDGSECVFVRKGVSEKIGGOKLEMSKTEAIK EFKRLFLEKTSNWEAEKTNPKOPGREYPLDVOYGVKAPKPKDKDISEMSKSLAPQ LLELMKMLFVETVRAAMEFEINNSEMPLGKLSKENIEKGFALTEIQNLKDTADQ ALAVRESLIVAAASNRFFTLIPSHPHIIROEDDMLKAKMLEALQDIEIASKIVGSDS DSDESLDDKMLHCDITPLAHSEDKLLIEQYLLNTHAPTHKDWLSLEVEFSLDRD GELNKYSRYKNLHNMKMLHSGRLTNFVGLSGLRLAPPEAPVTVTGMYGKGLYFAD LVKSAOYCYVDRNNPVGLMLSEVALGDMYELKATSMKPPRGKHSITGLKTKVPL ESEFVKRRDDVVPCGKVPSPSSIRSELNEXIYNTSVQKMQFLKVRFHHR"

BASE COUNT 968 a 604 c 813 g 826 t

ORIGIN

Query Match 100.0%; Score 474; DB 8; Length 3211; Best Local Similarity 100.0%; Pred. No. 9.2e-139; Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aacaagatgctattatggcagcgggttcagggttgacgaattttgtgggaattcttagtcaa 60  
DB 2549 AACAAAGATGCTATTATGACACGGTTCAAGGTTGACGAATTTGTGGGAATCTTAGTCAA 2608

QY 61 ggggttaagattgacacctctgagcagcctgttactggtctatatgttcggcaaggcctc 120  
DB 2609 GGGCTAAGAAATGACCTCCTGAGCACCTGTTACTGGCTATATGTTGGCAAAAGGCCTC 2668

QY 121 tactttgcagatcttagtaagcagcagcgaataacttactgttgaggaataaactct 180  
DB 2669 TACTTTGCAGATCTAGTAGCAAGAGCGACCAATACTGTTAGTGATAGGAATAATCCT 2728

QY 181 gtagggttgatgctctcttctgaggttcttaggagacatgtatgaactaaagaaagcc 240  
DB 2729 GTAGGTTTGCATGCTCTTCTGAGCTTGCTTTAGGAGACATGTATGAACCTAAAGAACCC 2788

QY 241 acgtcatgacaaacctccaaagagggaagcattcagcgaaggattgagcaaacctgt 300  
DB 2789 ACGTCCATGACAAACCTCCAAAGAGGGAAGCATTCGACCAAGGATTAGGCAAAACCGTG 2848

QY 301 ccactgagtcagagtttgaatggaggaggaatactgtagttccctgagcgaagccg 360  
DB 2849 CCACGTGAGTCAGAGTTTGTGAAGTGGAGGATGATGTCGTAGTTCCTCGGCAAGCCG 2908

QY 361 gtgcatcatcaataggagctctgaactcatgatacagatgagcatgctcacaacaca 420  
DB 2909 GTGCCATCAATATTAGGAGCTCTGAACCTCATGTACATGATGATCATGCTTACACACA 2968

QY 421 tcccaggtagaagatgagttctgtgtagaggttcgtttccatcacaagaggtag 474  
DB 2969 TCCCAGGTGAAGATGAGTCTTGTGCTGAAGGTGCGCTTTCCATCATCAAGAGGTAG 3022

RESULT 2

AF093627 3285 bp mRNA PLN 29-NOV-1998

LOCUS Zea mays poly(ADP-ribose) polymerase (PARP1) mRNA, complete cds.

DEFINITION AF093627

ACCESSION AF093627

VERSION AF093627.1 GI:3928870

KEYWORDS Zea mays.

SOURCE Zea mays.

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 3285) Mahajan, P.B. and Zuo, Z. Purification and cDNA cloning of maize Poly(ADP-ribose) polymerase Plant Physiol. 118 (3), 893-905 (1999)

AUTHORS Mahajan, P.B. and Zuo, Z.

TITLE Direct Submission

JOURNAL Submitted (22-SEP-1998) Crop Protection, Pioneer HiBred International, Inc., 7300 NW 62nd Avenue, Johnston, IA 50131-1004, USA

FEATURES

source Location/Qualifiers

1. .3285 /organism="Zea mays" /db\_xref="taxon:4577" 1. .3285 /gene="PARP1" 100. .3042 /gene="PARP1" /EC\_number="2.4.2.30" /function="add ADP-ribose" /codon\_start=1 /product="poly(ADP-ribose) polymerase" /protein\_id="AAC79704.1" /db\_xref="GI:3928871" /translation="MAAPKAWAEYAKSGRACKSCRSPIAKDQLRLGKMWQASQFD GFPMNHNHARCTFESKKNQIKSVSDVDDGIDALRWDDQEKIRNYVGSASAGTSTAAPPE KCTIETAPARTSCRCSEKTKGSRVLSAKLESSEKPGKIPWYHANCFFEVSPSATVE KFSWDTLSDERKMTDLVLDVKNQNEQNSKGRKKSENDIDSVKARLDESTSEGVNKGGLVDPDRGSNTSSADIDQLKKEQSDTLKLDGLKTHVSAELRDLMEANGQDTS GERHLLDRCADGMLPCANGMYIYNGYOCSGNVSEWSEKCTISATEPVRVKKWQIPGRTKNDYLMKWFQSKVPKPEVLPMPSPKSGSKATQRTSLSSKGLDKLRVSVVQSKKEANAEYRKARLKIPIVREGYIGE CVKKNKMLPFDLYKLENALSSKSTVTYVVKGRSAVHESGSLQDTAHILEDKSIYN ATLNMSDLALGVNSYYVLIQIEQDDGSECVFVRKGVSEKIGGOKLEMSKTEAIK EFKRLFLEKTSNWEAEKTNPKOPGREYPLDVOYGVKAPKPKDKDISEMSKSLAPQ LLELMKMLFVETVRAAMEFEINNSEMPLGKLSKENIEKGFALTEIQNLKDTADQ ALAVRESLIVAAASNRFFTLIPSHPHIIROEDDMLKAKMLEALQDIEIASKIVGSDS DSDESLDDKMLHCDITPLAHSEDKLLIEQYLLNTHAPTHKDWLSLEVEFSLDRD GELNKYSRYKNLHNMKMLHSGRLTNFVGLSGLRLAPPEAPVTVTGMYGKGLYFAD LVKSAOYCYVDRNNPVGLMLSEVALGDMYELKATSMKPPRGKHSITGLKTKVPL ESEFVKRRDDVVPCGKVPSPSSIRSELNEXIYNTSVQKMQFLKVRFHHR"

BASE COUNT 1003 a 617 c 828 g 837 t

ORIGIN

Query Match 100.0%; Score 474; DB 8; Length 3285; Best Local Similarity 100.0%; Pred. No. 9.3e-139; Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aacaagatgctattatggcagcgggttcagggttgacgaattttgtgggaattcttagtcaa 60  
DB 2569 AACAAAGATGCTATTATGACACGGTTCAAGGTTGACGAATTTGTGGGAATCTTAGTCAA 2628

QY 61 ggggttaagattgacacctctgagcagcctgttactggtctatatgttcggcaaggcctc 120  
DB 2629 GGGCTAAGAAATGACCTCCTGAGCACCTGTTACTGGCTATATGTTGGCAAAAGGCCTC 2688

QY 121 tactttgcagatcttagtaagcagcagcgaataacttactgttgaggaataaactct 180

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BASE COUNT 968 a 604 c 813 g 826 t  
ORIGIN

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209 gagaar

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VERSION      ATLL3705.1  GI:4038490
KEYWORDS     ADP-ribosyltransferase; parp-1 gene; poly(ADP-ribose)
SOURCE       polymerase.
ORGANISM     Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE    1 (bases 1 to 3197)
              Kazmaier, M.
              Direct Submission
              Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie
              Vegetale Et De Microbiologie, Commissariat A L'energie Atomique,
              CEA Cadarache, Lab. De Radiobiol. Vegetale, Bat. 185, 13108 St.
              Paul-les-Durance, FRANCE
REFERENCE    2 (bases 1 to 3187)
              Doucet-Chabeaud, G. and Kazmaier, M.
              Unpublished
              Location/Qualifiers
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BASE COUNT
mat_peptide

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[illegible]

| RESULTS    |                      | 3                                     |
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| ATH131705  | ATH131705            | 3187 bp mRNA                          |
| LOCUS      | Arabidopsis thaliana | PLN                                   |
| DEFINITION | Arabidopsis thaliana | mRNA for poly(ADP-ribose) polymerase. |
| ACCESSION  | AT131705             |                                       |